



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/812,315

Source:

IFWO

Date Processed by STIC:

4/6/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/812,315

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics**
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 04/06/2004

PATENT APPLICATION: US/10/812,315

TIME: 10:51:23

Input Set : A:\Sequence Listing 81000.txt

Output Set: N:\CRF4\04062004\J812315.raw

4 <110> APPLICANT: Degussa AG
 6 <120> TITLE OF INVENTION: A process for producing L-amino acids using strains of the
 7 Enterobacteriaceae family
 9 <130> FILE REFERENCE: 020481 BT
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/812,315
 C--> 11 <141> CURRENT FILING DATE: 2004-03-30
 11 <160> NUMBER OF SEQ ID NOS: 4
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 32
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Synthetic sequence
 21 <220> FEATURE:
 W--> 22 <221> NAME/KEY: Primer
 23 <222> LOCATION: (1)..(32)
 24 <223> OTHER INFORMATION: galP1
 27 <400> SEQUENCE: 1
 28 cacaatctag ataaaccata ttggaggggca tc
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 25
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Synthetic sequence
 36 <220> FEATURE:
 W--> 37 <221> NAME/KEY: Primer
 38 <222> LOCATION: (1)..(25)
 39 <223> OTHER INFORMATION: galP2
 42 <400> SEQUENCE: 2
 43 gggaggaagc ttgggggagat taatc
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 1446
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Escherichia coli
 51 <220> FEATURE:
 W--> 52 <221> NAME/KEY: DNA fragment
 53 <222> LOCATION: (1)..(1446)
 54 <223> OTHER INFORMATION: PCR product
 57 <220> FEATURE:
 58 <221> NAME/KEY: CDS
 59 <222> LOCATION: (33)..(1427)
 60 <223> OTHER INFORMATION: galP coding region
 W--> 61 <400> SEQUENCE: 3
 62 cacaatctag ataaaccata ttggaggggca tc atg cct gac gct aaa aaa cag
 63 Met Pro Asp Ala Lys Lys Gln

Invalid
Response

Does Not Comply
Corrected Diskette Needed

<213> has
to be either
Artificially Unknown
OR Genus / Species.

Invalid
Response

Same error

32
Please see
item #10
ON error
summary
sheet.

25

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Input Set : A:\Sequence Listing 81000.txt

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64									1				5				
66	ggg	cgg	tca	aac	aag	gca	atg	acg	ttt	ttc	gtc	tgc	ttc	ctt	gcc	gct	101
67	Gly	Arg	Ser	Asn	Lys	Ala	Met	Thr	Phe	Phe	Val	Cys	Phe	Leu	Ala	Ala	
68			10						15				20				
70	ctg	gcg	gga	tta	ctc	ttt	ggc	ctg	gat	atc	ggg	gta	att	gct	ggc	gca	149
71	Leu	Ala	Gly	Leu	Leu	Phe	Gly	Leu	Asp	Ile	Gly	Val	Ile	Ala	Gly	Ala	
72		25					30					35					
74	ctg	ccg	ttt	att	gca	gat	gaa	ttc	cag	att	act	tcg	cac	acg	caa	gaa	197
75	Leu	Pro	Phe	Ile	Ala	Asp	Glu	Phe	Gln	Ile	Thr	Ser	His	Thr	Gln	Glu	
76	40					45						50				55	
78	tgg	gtc	gta	agc	tcc	atg	atg	ttc	ggg	gcg	gca	gtc	ggg	gcg	gtg	ggc	245
79	Trp	Val	Val	Ser	Ser	Met	Met	Phe	Gly	Ala	Ala	Val	Gly	Ala	Val	Gly	
80				60					65				70				
82	agc	ggc	tgg	ctc	tcc	ttt	aaa	ctc	ggg	cgc	aaa	aag	agc	ctg	atg	atc	293
83	Ser	Gly	Trp	Leu	Ser	Phe	Lys	Leu	Gly	Arg	Lys	Lys	Ser	Leu	Met	Ile	
84			75						80				85				
86	ggc	gca	att	ttg	ttt	gtt	gcc	ggg	tcg	ctg	ttc	tct	gcg	gct	gcg	cca	341
87	Gly	Ala	Ile	Leu	Phe	Val	Ala	Gly	Ser	Leu	Phe	Ser	Ala	Ala	Ala	Pro	
88			90					95				100					
90	aac	gtt	gaa	gta	ctg	att	ctt	tcc	cgc	gtt	cta	ctg	ggg	ctg	gcg	gtg	389
91	Asn	Val	Glu	Val	Leu	Ile	Leu	Ser	Arg	Val	Leu	Leu	Gly	Leu	Ala	Val	
92		105					110					115					
94	ggg	gtg	gcc	tct	tat	acc	gca	ccg	ctg	tac	ctc	tct	gaa	att	gcg	ccg	437
95	Gly	Val	Ala	Ser	Tyr	Thr	Ala	Pro	Leu	Tyr	Leu	Ser	Glu	Ile	Ala	Pro	
96	120				125					130					135		
98	gaa	aaa	att	cgt	ggc	agt	atg	atc	tcg	atg	tat	cag	ttg	atg	atc	act	485
99	Glu	Lys	Ile	Arg	Gly	Ser	Met	Ile	Ser	Met	Tyr	Gln	Leu	Met	Ile	Thr	
100				140					145				150				
102	atc	ggg	atc	ctc	ggg	gct	tat	ctt	tct	gat	acc	gcc	ttc	agc	tac	acc	533
103	Ile	Gly	Ile	Leu	Gly	Ala	Tyr	Leu	Ser	Asp	Thr	Ala	Phe	Ser	Tyr	Thr	
104			155						160				165				
106	ggg	gca	tgg	cgc	tgg	atg	ctg	ggg	gtg	att	atc	atc	ccg	gca	att	ttg	581
107	Gly	Ala	Trp	Arg	Trp	Met	Leu	Gly	Val	Ile	Ile	Ile	Pro	Ala	Ile	Leu	
108			170				175					180					
110	ctg	ctg	att	ggg	gtc	ttc	ttc	ctg	cca	gac	agc	cca	cgt	tgg	ttt	gcc	629
111	Leu	Leu	Ile	Gly	Val	Phe	Phe	Leu	Pro	Asp	Ser	Pro	Arg	Trp	Phe	Ala	
112		185				190					195						
114	gcc	aaa	cgc	cgt	ttt	gtt	gat	gcc	gaa	cgc	gtg	ctg	cta	cgc	ctg	cgt	677
115	Ala	Lys	Arg	Arg	Phe	Val	Asp	Ala	Glu	Arg	Val	Leu	Leu	Arg	Leu	Arg	
116	200				205					210			215				
118	gac	acc	agc	gcg	gaa	gcg	aaa	cgc	gaa	ctg	gat	gaa	atc	cgt	gaa	agt	725
119	Asp	Thr	Ser	Ala	Glu	Ala	Lys	Arg	Glu	Leu	Asp	Glu	Ile	Arg	Glu	Ser	
120			220					225				230					
122	ttg	cag	gtt	aaa	cag	agt	ggc	tgg	gcg	ctg	ttt	aaa	gag	aac	agc	aac	773
123	Leu	Gln	Val	Lys	Gln	Ser	Gly	Trp	Ala	Leu	Phe	Lys	Glu	Asn	Ser	Asn	
124			235				240					245					
126	ttc	cgc	cgc	gcg	gtg	ttc	ctt	ggc	gta	ctg	ttg	cag	gta	atg	cag	caa	821
127	Phe	Arg	Arg	Ala	Val	Phe	Leu	Gly	Val	Leu	Leu	Gln	Val	Met	Gln	Gln	
128			250				255					260					

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Input Set : A:\Sequence Listing 81000.txt

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```

130 ttc acc ggg atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa      869
131 Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu
132      265      270      275
134 ctg gcg ggt tat acc aac act acc gag caa atg tgg ggg acc gtg att      917
135 Leu Ala Gly Tyr Thr Asn Thr Thr Glu Gln Met Trp Gly Thr Val Ile
136 280      285      290      295
138 gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt      965
139 Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val
140      300      305      310
142 gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg      1013
143 Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met
144      315      320      325
146 gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac      1061
147 Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His
148      330      335      340
150 tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att      1109
151 Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile
152      345      350      355
154 gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc      1157
155 Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser
156 360      365      370      375
158 gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act      1205
159 Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr
160      380      385      390
162 gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc      1253
163 Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr
164      395      400      405
166 atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct      1301
167 Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala
168      410      415      420
170 ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc      1349
171 Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr
172      425      430      435
174 aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt      1397
175 Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg
176 440      445      450      455
178 aaa ctg cgc gaa ata ggc gct cac gat taa tctccccaag cttcctccc      1446
179 Lys Leu Arg Glu Ile Gly Ala His Asp
180      460
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 464
184 <212> TYPE: PRT
185 <213> ORGANISM: Escherichia coli
188 <400> SEQUENCE: 4
189 Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe
190 1      5      10      15
192 Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp
193      20      25      30
195 Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln

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196          35          40          45
198 Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
199          50          55          60
201 Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
202 65          70          75          80
204 Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
205          85          90          95
207 Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
208          100          105          110
210 Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
211          115          120          125
213 Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
214          130          135          140
216 Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
217 145          150          155          160
219 Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
220          165          170          175
222 Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro
223          180          185          190
225 Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
226          195          200          205
228 Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
229          210          215          220
231 Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
232 225          230          235          240
234 Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
235          245          250          255
237 Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
238          260          265          270
241 Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
242          275          280          285
244 Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
245          290          295          300
247 Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
248 305          310          315          320
250 Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
251          325          330          335
253 Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
254          340          345          350
256 Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
257          355          360          365
259 Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
260          370          375          380
262 Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
263 385          390          395          400
265 Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
266          405          410          415
268 Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
269          420          425          430

```

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271	Leu	Trp	Leu	Val	Pro	Glu	Thr	Lys	His	Val	Ser	Leu	Glu	His	Ile	Glu
272			435					440					445			
274	Arg	Asn	Leu	Met	Lys	Gly	Arg	Lys	Leu	Arg	Glu	Ile	Gly	Ala	His	Asp
275			450					455					460			

VERIFICATION SUMMARY

DATE: 04/06/2004

PATENT APPLICATION: US/10/812,315

TIME: 10:51:24

Input Set : A:\Sequence Listing 81000.txt

Output Set: N:\CRF4\04062004\J812315.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:37 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:52 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:61 M:283 W: Missing Blank Line separator, <400> field identifier